

FIG. 1A: Full length Intron A = 820 bp

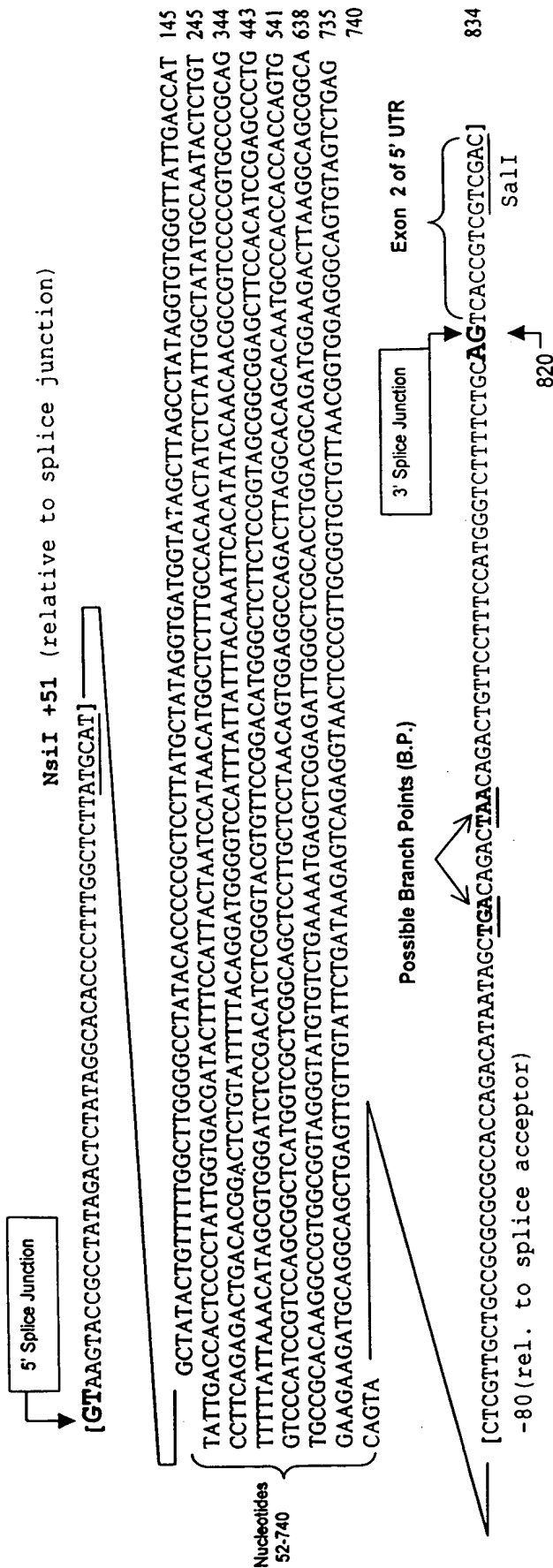


FIG. 1B: Synthetic Oligo for substitution of nucleotides 52-740 of Intron A

[ATGCATCTCGTTGCTGCCGCGCGCCACAGACATAATCGCTGACACACTGACAGACTGTTCCTTTTCTTTTTCAGTCCACCGTCGTCGAC]
NsiI -80
Changed to B.P. consensus
Changed to polypyrimidine consensus
Sali

FIG. 1C: Deletion Mutant pCON3 Intron: 132 bp

NsiI
Branch Point

[GTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCATCTGCTGGCGCGCCACAGACATAATCGCTGACACACTGA
CAGACTGTTCTCTTCTCTTTTCTTTTTCAGTCCACCGTCGTCGAC]
Polypyrimidine Tract
Sali

17:50 11:25:50

1 ctgcagtga taataaaatg tgtgtttgtc cgaaatacgc gttttgagat ttctgtcgcc
 61 gactaaattc atgtcgcgcg atagtgggtt ttatcgccga tagagatggc gatattggaa
 121 aaatcgatat ttgaaaatat ggcatattga aaatgtcgcc gatgtgagtt tctgtgtaac
 181 tgatatcgcc atttttccaa aagtgtttt tgggcatacg cgatatctgg cgatacggct
 241 tatatcgttt acgggggatg gcgatagacg actttggcga cttggggcat tctgtgtgtc
 301 gcaaatatcg cagtttcgat ataggtgaca gacgatatga ggctatatcg ccgatagagg
 361 cgacatcaag ctggcacatg gccaatgcat atcgatctat acattgaatc aatattggca
 421 attagccata ttagtcattg gttatatagc ataaatcaat attggctatt ggccattgca
 481 tacgttgtat ctatatcata atatgtacat ttatattggc tcatgtccaa tatgaccgcc
 541 atgttgacat tgattattga ctagtattta atagtaatca attacggggg cattagttca
 601 tagcccatat atggagtcc gcgttacata acttacggta aatggcccgc ctctgacccg
 661 cccaaacgacc cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccata
 721 gggactttcc attgacgtca atgggtggag tatttacggg aaactgccc cttggcagta
 781 catcaagtgt atcatatgcc aagtcgggcc ccctattgac gtcaatgacg gtaaatggcc
 841 cgcttgcat tatgccagc acatgacctt acgggacttt cctacttggc agtacatcta
 901 cgtattagtc atcgctatta ccattggtgat gcggttttgg cagtacacca atgggcgtgg
 961 atagcgggtt gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt
 1021 gttttggcac caaaatcaac gggactttcc aaaatgtcgt aataacccc ccccggtgac
 1081 g⁺caaatgggc ggtaggcgtg tacggtggga ggtcta⁺tata agcagagctc gtttagtgaa
 1141 ccg⁺tcagatc gcctggagac gccatccacg ctgttttgac ctccatagaa gacaccggga
 1201 ccgatccagc ctccgcgcc gggaacggg cattggaacg cggattcccc gtgccaagag
 1261 tgacGTAAGT ACCGCCTATA GACTCTATAG GCACACCCCT TTGGCTCTTA TGCATGCTAT
 1321 ACTGTTTTTG GCTTGGGGCC TATACACCCC CGCTCCTTAT GCTATAGGTG ATGGTATAGC
 1381 TTAGCCTATA GGTGTGGGTT ATTGACCATT ATTGACCACT CCCCTATTGG TGACGATACT
 1441 TTCCATTACT AATCCATAAC ATGGCTCTTT GCCACAATA TCTCTATTGG CTATATGCCA
 1501 ATACTCTGTC CTTGAGAGAC TGACACGGAC TCTGTATTTT TACAGGATGG GGTCCCATTT
 1561 ATTATTTACA AATTCACATA TACAACAACG CCGTCCCCCG TGCCCGCAGT TTTTATTAAA
 1621 CATAGCGTGG GATCTCCACG CGAATCTCGG GTACGTGTTT CGGACATGGG CTCTTCTCCG
 1681 GTAGCGGCGG AGCTTCCACA TCCGAGCCCT GGTCCCATGC CTCCAGCGGC TCATGGTCGC
 1741 TCGGCAGCTC CTTGCTCCTA ACAGTGGAGG CCAGACTTAG GCACAGCACA ATGCCACCA
 1801 CCACCAGTGT GCCGCACAAG GCCGTGGCGG TAGGGTATGT GTCTGAAAAT GAGCTCGGAG
 1861 ATTGGGCTCG CACCGTGACG CAGATGGAAG ACTTAAGGCA GCGGCAGAAG AAGATGCAGG
 1921 CAGCTGAGTT GTTGTATTCT GATAAGAGTC AGAGGTAAC CCCGTTGCCG TGCTGTAAAC
 1981 GGTGGAGGGC AGTGTAGTCT GAGCAGTACT CGTTGCTGCC GCGCGGCCA CCAGACATAA
 2041 TAGCTGACAG ACTAACAGAC TGTTCTTTC CATGGGTCTT TTCTGCAGtc accgtccttg
 2101 acacgatgga gtcctctgcc aagagaaag⁺tg⁺gaccctga taatcctgac gagggccctt
 2161 cctccaaggt

Enhancer Region
 (~600 - ~1081)

Pol II Promoter
 (1081 - 1143)

Exon 1 (5' UTR)
 (1144 - 1264)

Intron A
 (1265 - 2088)

Exon 2 (5' UTR,
 Start of Tr.)
 (2089 -)

FIG. 2

Deletions Made Within Intron A of CMV IE1

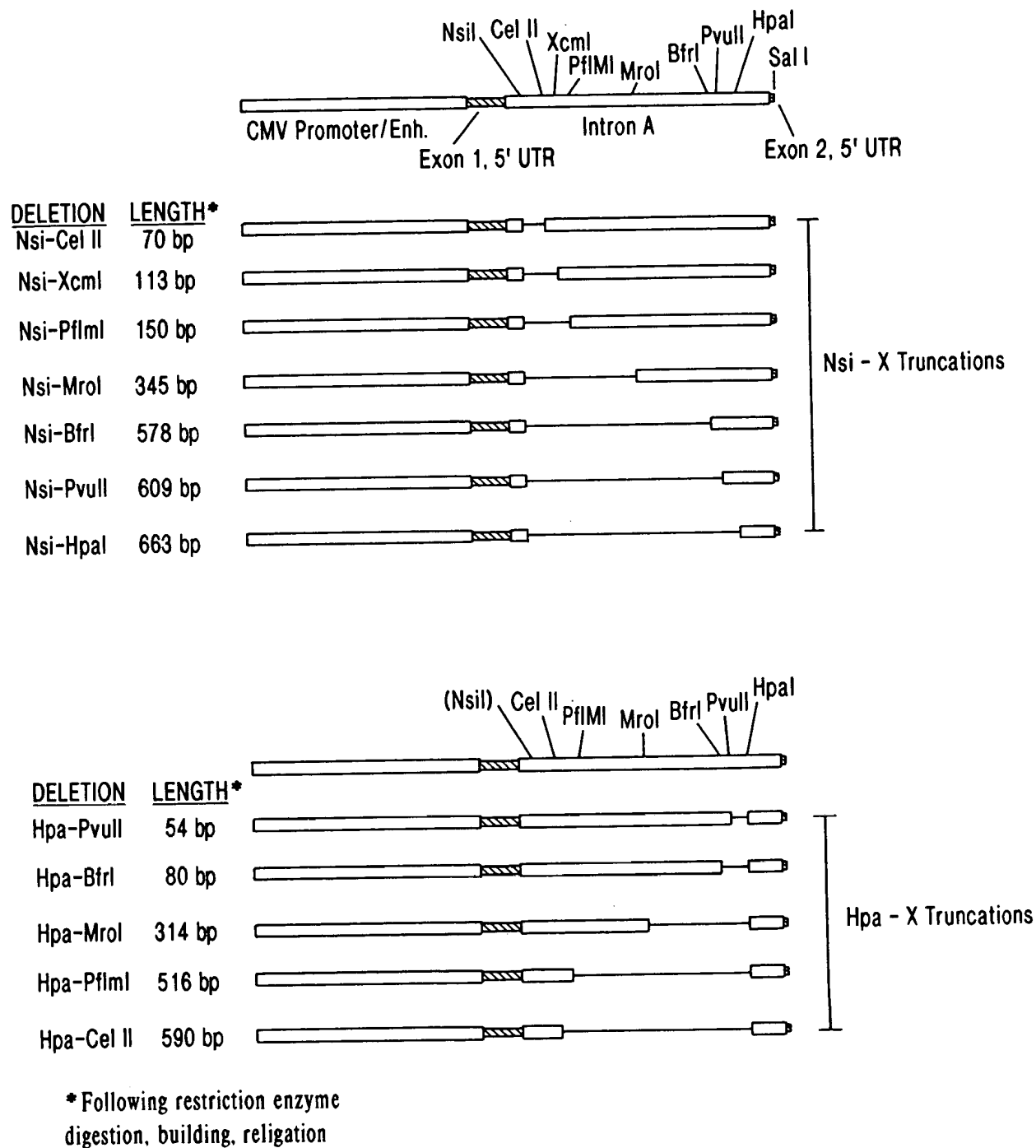
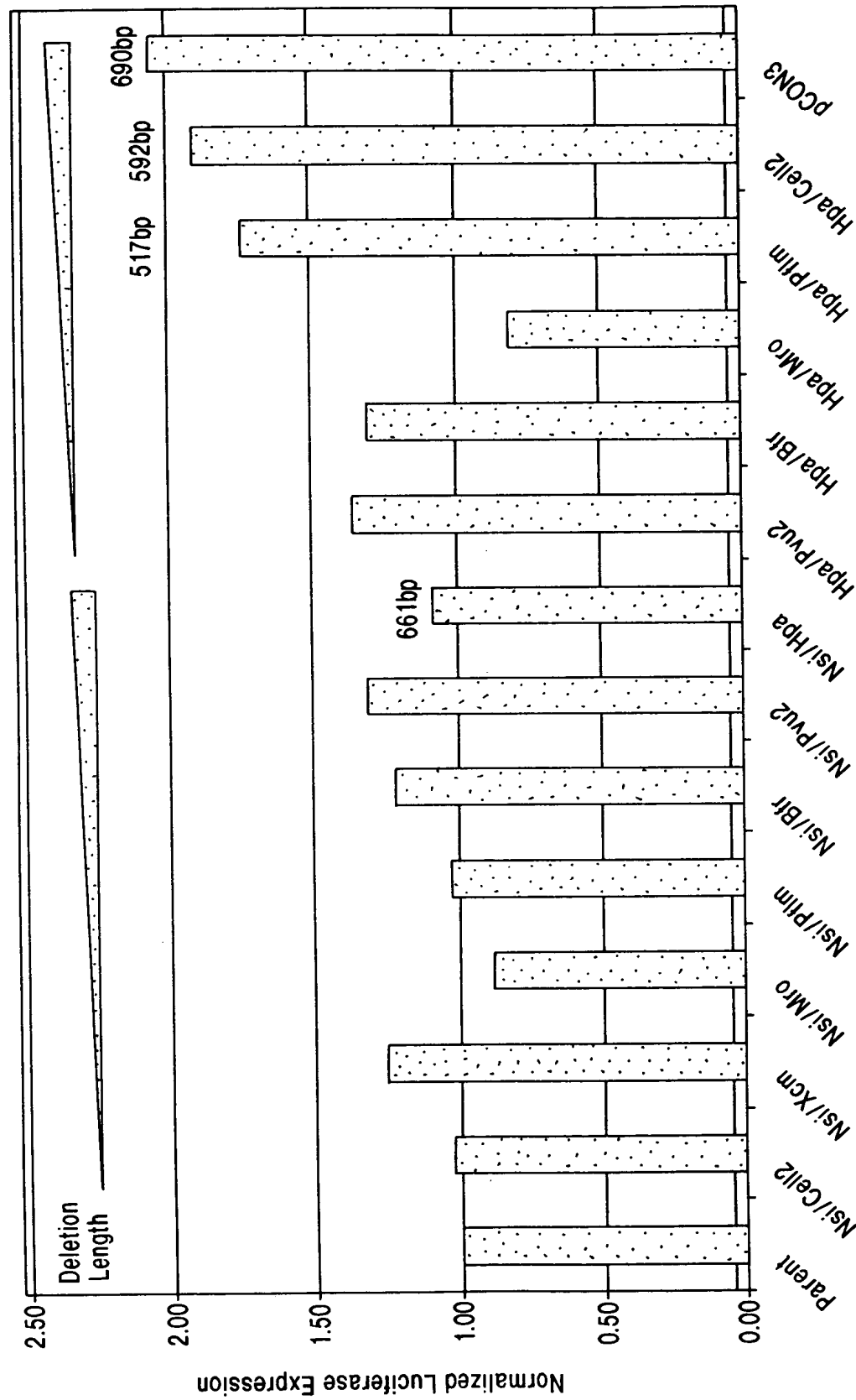


FIG. 3

Intron A Internal Deletion Mutants
(Transiently-Transfected 293 cells)



Construct I.D.

FIG. 4

1. Wild Type Rabbit β -Globin Sequence

GTTGGTATCCTTTTTACAGCACAACCTTAATGAGACAGATAGAACTGGTCTTGTAGAAACA
Splice Donor

GAGTAGTCGCCTGCTTTTCTGCCAGGTGTCTGACTTCTCTCCCCTGGGCTGTTTTCATTTTCTCAG
Branch Pt. Polypyrimidine Tract

FIG. 5A

2. Optimized Rabbit β -Globin Sequence

GTAAGTATCCTTTTTACAGCACAACCTTAATGAGACAGATAGAACTGGTCTTGTAGAAACA
Splice Donor

GAGTAGTCGCCTGCTTTTCTGCCAGGTACTAACTTCTCTCCCCTCTCCTCTTTTCTTTTCTGCAG
Branch Pt. Polypyrimidine Tract

FIG. 5B

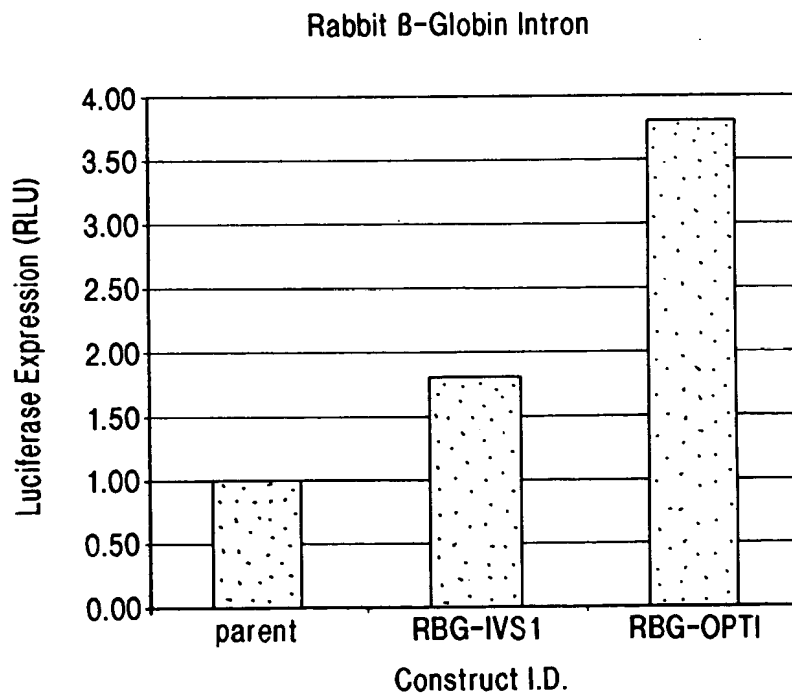


FIG. 6

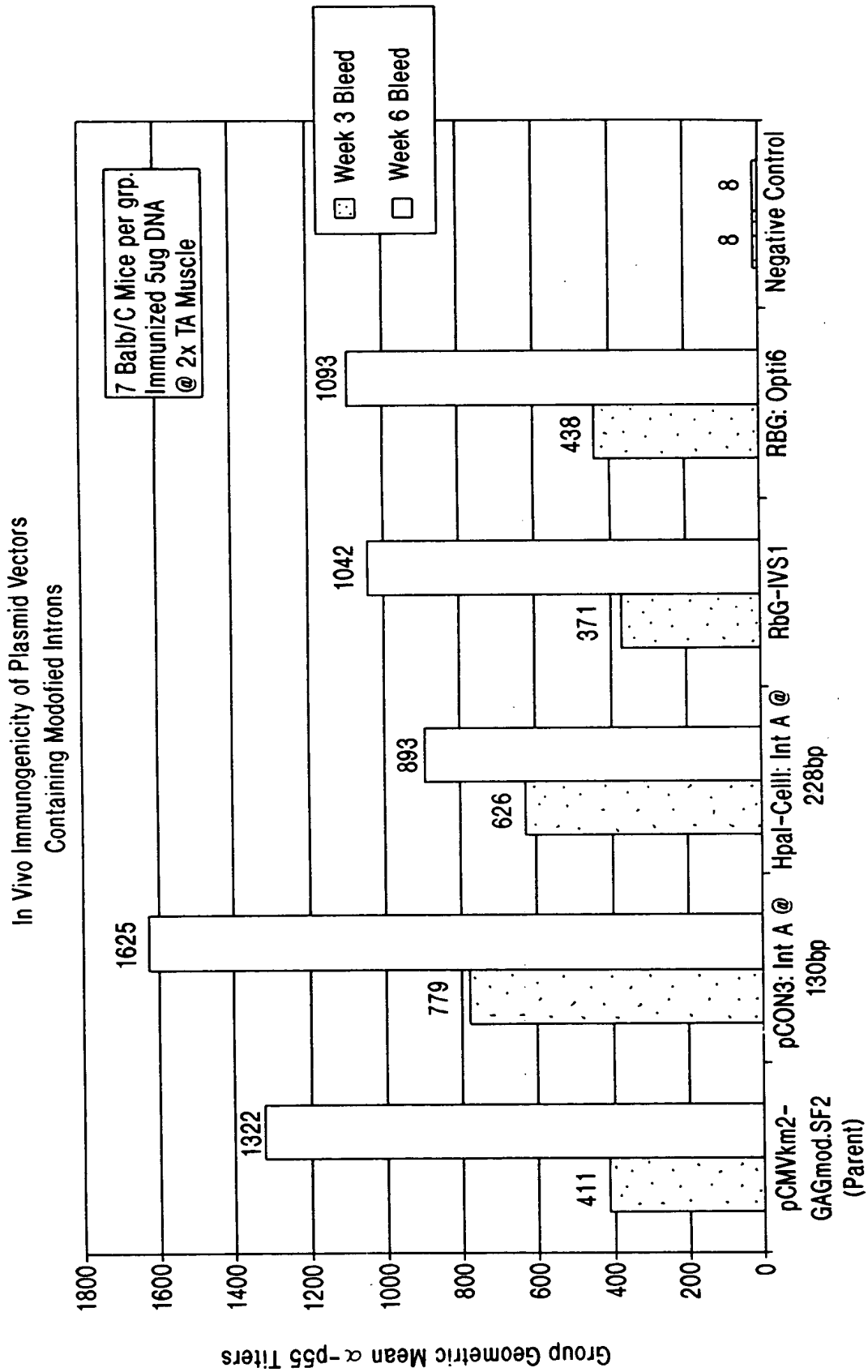


FIG. 7